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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/900,963	07/10/2001	Claudine Guerin-Marchand	010830-118	8667

21839	7590	04/04/2006

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EXAMINER
LUCAS, ZACHARIAH

ART UNIT	PAPER NUMBER
1648	

DATE MAILED: 04/04/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

PTO-90C (Rev. 10/03)

APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.

EXAMINER

ART UNIT	PAPER

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.
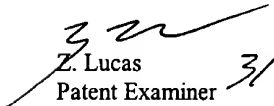
Commissioner for Patents

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth below or on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. **Neither the paper copy, nor the computer readable form (CRF) of the sequence listings complies with the sequence rules for the reasons indicated in the attached RAW SEQUENCE LISTING ERROR REPORT.**

Applicant is given ONE MONTH, or THIRTY DAYS, whichever is longer, from the mailing date of this letter within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). In no case may an applicant extend the period for reply beyond the SIX MONTH statutory period. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Zachariah Lucas whose telephone number is 571-272-0905. The examiner can normally be reached on Monday-Friday, 8 am to 4:30 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, James Housel can be reached on 571-272-0902. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Z. Lucas 3/31/06
Patent Examiner

Note- attached Raw Sequence
Listing Error Report

PTO-90C (Rev.04-03)

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
   ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _09/900, 963 B_
Source: _JFW/6_
Date Processed by STIC: _12/15/2005_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
      http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio **(<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission
   User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/24/05

)

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/900, 963B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
     Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino
     Numbering — The numbering under each 5th amino acid is misaligned. **Do not use tab codes between numbers; use space characters, instead.**

4____Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5____Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
     "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
     (OLD RULES)
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include the skipped sequences.**

8____Skipped Sequences — Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
     (NEW RULES)
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's — Use of n's and/or Xaa's have been detected in the Sequence Listing.
     (NEW RULES) — Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>
     Response — Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11____Use of <220> — ~~Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.~~
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
     "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

IFW16

RAW SEQUENCE LISTING   DATE: 12/15/2005
PATENT APPLICATION: US/09/900,963B   TIME: 08:47:31

Input Set : N:\Crf4\Refhold\09_folder\I900963B.raw
Output Set: N:\CRF4\12152005\I900963B.raw

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     1 <110> APPLICANT: GUERIN-MARCHAND, CLAUDINE
     2       DRUILHE, PIERRE
     3 <120> TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE HEPATIC STAGES OF P.
FALCIPARUM
     4       BEARING EPITOPES CAPABLE OF STIMULATING THE T LYMPHOCYTES
     5 <130> FILE REFERENCE: 010830-118
C--> 6 <140> CURRENT APPLICATION NUMBER: US/09/900,963B
     7 <141> CURRENT FILING DATE: 2001-07-10
     8 <150> PRIOR APPLICATION NUMBER: 08/098,327
     9 <151> PRIOR FILING DATE: 1993-11-24
    10 <150> PRIOR APPLICATION NUMBER: PCT/FR92/00104
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    14 <160> NUMBER OF SEQ ID NOS: 47
    15 <170> SOFTWARE: PatentIn Ver. 3.3
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pp 1-2, 5, 7

*Does Not Comply
Corrected Diskette Needed*

ERRORED SEQUENCES

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   769 <211> LENGTH: 954
   770 <212> TYPE: DNA
   771 <213> ORGANISM: Plasmodium falciparum
   772 <221> NAME/KEY: CDS
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   777        1               5                   10                  15
   778       ttg ata ttt cat ata aat gga aag ata ata aag aat tct gaa aaa gat    96
   779       Leu Ile Phe His Ile Asn Gly Lys Ile Ile Lys Asn Ser Glu Lys Asp
   780                        20                  25                  30
   781       gaa atc ata aaa tct aac ttg aga agt ggt tct tca aat tct agg aat   144
   782       Glu Ile Ile Lys Ser Asn Leu Arg Ser Gly Ser Ser Asn Ser Arg Asn
   783                    35                  40                  45
   784       cga ata aat gag gaa aat cac gag aag aaa cac gtt tta tct cat aat   192
   785       Arg Ile Asn Glu Glu Asn His Glu Lys Lys His Val Leu Ser His Asn
   786            50                  55                  60
   787       tca tat gag aaa act aaa aat aat gaa aat aat aaa ttt ttc gat aag   240
   788       Ser Tyr Glu Lys Thr Lys Asn Asn Glu Asn Asn Lys Phe Phe Asp Lys
   789            65                  70                  75                  80
   790       gat aaa gag tta acg atg tct aat gta aaa aat gtg tca caa aca aat   288
   791       Asp Lys Glu Leu Thr Met Ser Asn Val Lys Asn Val Ser Gln Thr Asn
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Insert <220> whenever <221>, <222> or <223> is

Sharon <220> never has a response or it is a header only.

RAW SEQUENCE LISTING   DATE: 12/15/2005
PATENT APPLICATION: US/09/900,963B   TIME: 08:47:31

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Output Set: N:\CRF4\12152005\I900963B.raw

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795                    100               105                   110
796        aaa gaa aat aaa tta aat aag gaa ggg aaa tta att gaa cac ata ata   384
797        Lys Glu Asn Lys Leu Asn Lys Glu Gly Lys Leu Ile Glu His Ile Ile
798                    115               120               125
799        aat gat gat gac gat aaa aaa aaa tat att aaa ggg caa gac gaa aac   432
800        Asn Asp Asp Asp Asp Lys Lys Lys Tyr Ile Lys Gly Gln Asp Glu Asn
801             130               135               140
802        aga caa gaa gat ctt gaa gaa aaa gca gct aaa gaa aag tta cag ggg   480
803        Arg Gln Glu Asp Leu Glu Glu Lys Ala Ala Lys Glu Lys Leu Gln Gly
804        145               150               155               160
805        caa caa agc gat tca gaa caa gag aga cgt gct aaa gaa aag ttg caa   528
806        Gln Gln Ser Asp Ser Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln
807                    165               170               175
808        gaa caa caa agc gat tta gaa caa gag aga ctt gct aaa gaa aag ttg   576
809        Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys Glu Lys Leu
810                    180               185               190
811        caa gaa caa caa agc gat tta gaa caa gag aga cgt gct aaa gaa aag   624
812        Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys
813             195               200               205
814        ttg caa gaa caa caa agc gat tta gaa caa gag aga ctt gct aaa gaa   672
815        Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys Glu
816        210               215               220
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818        Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys
819        225               230               235               240
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824        Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu
825                    260               265               270
826        gct aaa gaa aag tta caa gag cag caa agc gat tta gaa caa gat aga   864
827        Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg
828             275               280               285
829        ctt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag   912
830        Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu
831             290               295               300
832        aga cgt gct aaa gaa agg ttg caa gaa caa caa agc gat tta           954
833        Arg Arg Ala Lys Glu Arg Leu Gln Glu Gln Gln Ser Asp Leu
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928  <211> LENGTH: 1494
929  <212> TYPE: DNA
930  <213> ORGANISM: Plasmodium falciparum
931  <221> NAME/KEY: CDS
932  <222> LOCATION: (1)..(1494)
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RAW SEQUENCE LISTING   DATE: 12/15/2005
PATENT APPLICATION: US/09/900,963B   TIME: 08:47:31

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     938     Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu
     939                    20                  25                  30
     940     aag tta caa gag cag caa agc gat tta gaa caa gag aga ctt gct aaa   144
     941     Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys
     942             35                  40                  45
     943     gaa aag ttg caa gaa caa caa agc gat cta gaa caa gag aga cgt gct   192
     944     Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala
     945          50                  55                  60
     946     aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag aga cgt   240
     947     Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg
     948      65                  70                  75                  80
     949     gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gat aga   288
     950     Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg
     951                    85                  90                  95
     952     ctt gct aaa gaa aag tta caa gag cag caa agc gat tta gaa caa gag   336
     953     Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu
     954                   100                 105                 110
     955     aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa   384
     956     Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln
     957             115                 120                 125
     958     gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa   432
     959     Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu
     960          130                 135                 140
     961     caa gag aga ctt gct aaa gaa aag ttg caa gaa caa caa agc gat tta   480
     962     Gln Glu Arg Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu
     963     145                 150                 155                 160
     964     gaa caa gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat   528
     965     Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp
     966                   165                 170                 175
     967     tta gaa caa gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc   576
     968     Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser
     969                   180                 185                 190
     970     gat tta gaa caa gag aga cgt gct aaa gaa aag ttg caa gag cag caa   624
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     973     aga gat tta gaa caa agg aag gct gat acg aaa aaa aat tta gaa aga   672
     974     Arg Asp Leu Glu Gln Arg Lys Ala Asp Thr Lys Lys Asn Leu Glu Arg
     975          210                 215                 220
     976     aaa aag gaa cat gga gat ata tta gca gag gat tta tat ggt cgt tta   720
     977     Lys Lys Glu His Gly Asp Ile Leu Ala Glu Asp Leu Tyr Gly Arg Leu
     978     225                 230                 235                 240
     979     gaa ata cca gct ata gaa ctt cca tca gaa aat gaa cgt gga tat tat   768
     980     Glu Ile Pro Ala Ile Glu Leu Pro Ser Glu Asn Glu Arg Gly Tyr Tyr
     981                   245                 250                 255
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982      ata cca cat caa tct tct tta cct cag gac aac aga ggg aat agt aga    816
983      Ile Pro His Gln Ser Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg
984                  260             265             270
985      gat tcc aag gaa ata tct ata ata gaa aaa aca aat aga gaa tct att    864
986      Asp Ser Lys Glu Ile Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile
987                  275             280             285
988      aca aca aat gtt gaa gga cga agg gat ata cat aaa gga cat ctt gaa    912
989      Thr Thr Asn Val Glu Gly Arg Arg Asp Ile His Lys Gly His Leu Glu
990          290             295             300
991      gaa aag aaa gat ggt tca ata aaa cca gaa caa aaa gaa gat aaa tct    960
992      Glu Lys Lys Asp Gly Ser Ile Lys Pro Glu Gln Lys Glu Asp Lys Ser
993      305             310             315             320
994      gct gac ata caa aat cat aca tta gag aca gta aat att tct gat gtt    1008
995      Ala Asp Ile Gln Asn His Thr Leu Glu Thr Val Asn Ile Ser Asp Val
996                  325             330             335
997      aat gat ttt caa ata agt aag tat gag gat gaa ata agt gct gaa tat    1056
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1007     Gly Ile Tyr Lys Glu Leu Glu Asp Leu Ile Glu Lys Asn Glu Asn Leu
1008     385             390             395             400
1009     gat gat tta gat gaa gga ata gaa aaa tca tca gaa gaa tta tct gaa    1248
1010     Asp Asp Leu Asp Glu Gly Ile Glu Lys Ser Ser Glu Glu Leu Ser Glu
1011                 405             410             415
1012     gaa aaa ata aaa aaa gga aag aaa tat gaa aaa aca aag gat aat aat    1296
1013     Glu Lys Ile Lys Lys Gly Lys Lys Tyr Glu Lys Thr Lys Asp Asn Asn
1014                 420             425             430
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1017                 435             440             445
1018     aaa aat gat aag cag gtt aat aag gaa aag gaa aaa ttc ata aaa tca    1392
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1024     gag tta tct gaa gat ata act aaa tat ttt atg aaa cta taa aag gtt    1488
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1120      1               5               10                  15
1121      ttg caa gaa caa caa agc gat tta gaa caa gat aga ctt gct aaa gaa   96
1122      Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu
1123                      20              25                  30
1124      aag tta caa gag cag caa agc gat tta gaa caa gag aga ctt gct aaa   144
1125      Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Leu Ala Lys
1126              35              40                  45
1127      gaa aag ttg caa gaa caa caa agc gat cta gaa caa gag aga cgt gct   192
1128      Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala
1129              50              55                  60
1130      aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gag aga cgt   240
1131      Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg
1132      65              70                  75                  80
1133      gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa gat aga   288
1134      Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Asp Arg
1135                      85              90                  95
1136      ctt gct aaa gaa aag tta caa gag cag caa agc gat tta gaa caa gag   336
1137      Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu
1138              100             105                 110
1139      aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa caa   384
1140      Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln
1141              115             120                 125
1142      gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat tta gaa   432
1143      Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu
1144              130             135                 140
1145      caa gag aga ctt gct aaa gaa aag ttg caa gaa caa caa agc gat tta   480
1146      Gln Glu Arg Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu
1147      145             150                 155                 160
1148      gaa caa gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc gat   528
1149      Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp
1150                      165                 170                 175
1151      tta gaa caa gag aga cgt gct aaa gaa aag ttg caa gaa caa caa agc   576
1152      Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser
1153                      180                 185                 190
1154      gat tta gaa caa gag aga cgt gct aaa gaa aag ttg caa gag cag caa   624
1155      Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln
1156              195                 200                 205
1157      aga gat tta gaa caa agg aag gct gat acg aaa aaa aat tta gaa aga   672
1158      Arg Asp Leu Glu Gln Arg Lys Ala Asp Thr Lys Lys Asn Leu Glu Arg
1159              210                 215                 220
1160      aaa aag gaa cat gga gat ata tta gca gag gat tta tat ggt cgt tta   720
1161      Lys Lys Glu His Gly Asp Ile Leu Ala Glu Asp Leu Tyr Gly Arg Leu
1162      225                 230                 235                 240
```

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1163    gaa ata cca gct ata gaa ctt cca tca gaa aat gaa cgt gga tat tat    768
1164    Glu Ile Pro Ala Ile Glu Leu Pro Ser Glu Asn Glu Arg Gly Tyr Tyr
1165                245                 250                 255
1166    ata cca cat caa tct tct tta cct cag gac aac aga ggg aat agt aga    816
1167    Ile Pro His Gln Ser Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg
1168                260                 265                 270
1169    gat tcc aag gaa ata tct ata ata gaa aaa aca aat aga gaa tct att    864
1170    Asp Ser Lys Glu Ile Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile
1171            275                 280                 285
1172    aca aca aat gtt gaa gga cga agg gat ata cat aaa gga cat ctt gaa    912
1173    Thr Thr Asn Val Glu Gly Arg Arg Asp Ile His Lys Gly His Leu Glu
1174            290                 295                 300
1175    gaa aag aaa gat ggt tca ata aaa cca gaa caa aaa gaa gat aaa tct    960
1176    Glu Lys Lys Asp Gly Ser Ile Lys Pro Glu Gln Lys Glu Asp Lys Ser
1177    305                 310                 315                 320
1178    gct gac ata caa aat cat aca tta gag aca gta aat att tct gat gtt    1008
1179    Ala Asp Ile Gln Asn His Thr Leu Glu Thr Val Asn Ile Ser Asp Val
1180                325                 330                 335
1181    aat gat ttt caa ata agt aag tat gag gat gaa ata agt gct gaa tat    1056
1182    Asn Asp Phe Gln Ile Ser Lys Tyr Glu Asp Glu Ile Ser Ala Glu Tyr
1183                340                 345                 350
1184    gac gat tca tta ata gat gaa gaa gaa gat gat gaa gac tta gac gaa    1104
1185    Asp Asp Ser Leu Ile Asp Glu Glu Glu Asp Asp Glu Asp Leu Asp Glu
1186            355                 360                 365
1187    ttt aag cct att gtg caa tat gac aat ttc caa gat gaa gaa aac ata    1152
1188    Phe Lys Pro Ile Val Gln Tyr Asp Asn Phe Gln Asp Glu Glu Asn Ile
1189            370                 375                 380
1190    gga att tat aaa gaa cta gaa gat ttg ata gag aaa aat gaa aat tta    1200
1191    Gly Ile Tyr Lys Glu Leu Glu Asp Leu Ile Glu Lys Asn Glu Asn Leu
1192    385                 390                 395                 400
1193    gat gat tta gat gaa gga ata gaa aaa tca tca gaa gaa tta tct gaa    1248
1194    Asp Asp Leu Asp Glu Gly Ile Glu Lys Ser Ser Glu Glu Leu Ser Glu
1195                405                 410                 415
1196    gaa aaa ata aaa aaa gga aag aaa tat gaa aaa aca aag gat aat aat    1296
1197    Glu Lys Ile Lys Lys Gly Lys Lys Tyr Glu Lys Thr Lys Asp Asn Asn
1198                420                 425                 430
1199    ttt aaa cca aat gat aaa agt ttg tat gat gag cat att aaa aaa tat    1344
1200    Phe Lys Pro Asn Asp Lys Ser Leu Tyr Asp Glu His Ile Lys Lys Tyr
1201            435                 440                 445
1202    aaa aat gat aag cag gtt aat aag gaa aag gaa aaa ttc ata aaa tca    1392
1203    Lys Asn Asp Lys Gln Val Asn Lys Glu Lys Glu Lys Phe Ile Lys Ser
1204            450                 455                 460
1205    ttg ttt cat ata ttt gac gga gac aat gaa att tta cag atc gtg gat    1440
1206    Leu Phe His Ile Phe Asp Gly Asp Asn Glu Ile Leu Gln Ile Val Asp
1207    465                 470                 475                 480
1208    gag tta tct gaa gat ata act aaa tat ttt atg aaa cta taa aag gtt    1488
1209    Glu Leu Ser Glu Asp Ile Thr Lys Tyr Phe Met Lys Leu
1210                485                 490
1211    ata tat    1494
```

<210> 1
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Formula Sequence

Insufficient Explanation. Give Source(s) of genetic material (see item 11 on Error Summary Sheet).

<220>
<221> VARIANT
<222> 8
<223> Xaa = Glu or Gly

<400> 1
Leu Ala Lys Glu Lys Leu Gln Xaa Gln Gln Ser Asp Leu Glu Gln Glu
 1   5   10   15
Arg

The above is a Sample of Global Error

P41

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/15/2005
PATENT APPLICATION: US/09/900,963B   TIME: 08:47:32

Input Set : N:\Crf4\Refhold\09_folder\I900963B.raw
Output Set: N:\CRF4\12152005\I900963B.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 3

VERIFICATION SUMMARY   DATE: 12/15/2005
PATENT APPLICATION: US/09/900,963B   TIME: 08:47:32

Input Set : N:\Crf4\Refhold\09_folder\I900963B.raw
Output Set: N:\CRF4\12152005\I900963B.raw

```
L:6 M:270 C: Current Application Number differs, Wrong Format
L:28 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:38 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:16
L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:16
L:325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:16
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:460 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:16
L:774 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:37
L:933 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:42
L:1117 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:46
```